

## SEQUENCE LISTING

<110> National Institute of Advanced Industrial Science and Technology

<120> Gene and peptide for transcriptional repressor

<130> PH-1684-PCT

<150> JP 2001-395487

<151> 2001-12-26

<150> JP 2001-395488

<151> 2001-12-26

<150> JP 2002-160671

<151> 2002-5-31

<160> 118

<210> 1

<211> 12

<212> PRT

<213> Nicotiana tabacum

<400> 1

Asp Leu Asp Leu Asn Leu Ala Pro Pro Met Glu Phe

1

5

10

<210> 2

<211> 41

<212> DNA

<213> Nicotiana tabacum

<400> 2

cgatcttgat cttaaccttg ctccacctat ggaatttga g

41

<210> 3

<211> 45

<212> DNA

<213> Nicotiana tabacum

<400> 3

tcgactcaaa attccatagg tggagcaagg ttaagatcaa gatcg

45

<210> 4

<211> 11

<212> PRT

<213> artificial

<400> 4

Leu Asp Leu Asn Leu Ala Pro Pro Met Glu Phe

1

5

10

<210> 5

<211> 38

<212> DNA

<213> artificial

<400> 5

ccttgatctt aaccttgctc cacctatgga attttgag

38

<210> 6

<211> 42

<212> DNA

<213> artificial

<400> 6

tcgactcaaa attccatagg tggagcaagg ttaagatcaa gg

42

<210> 7

<211> 11

<212> PRT

<213> artificial

<400> 7

Leu Asp Leu Asn Leu Ala Ala Ala Ala Ala Ala

1

5

10

<210> 8

<211> 38

<212> DNA

<213> artificial

<400> 8

ccttgatctt aaccttgctg ctgctgctgc tgcttgag

38

<210> 9

<211> 42

<212> DNA

<213> artificial

<400> 9

tcgactcaag cagcagcagc agcagcaagg ttaagatcaa gg

42

<210> 10

<211> 4

<212>PRT

<213> Arabidopsis thaliana

<400> 10

Leu Asp Leu Asn

<210> 11

<211> 17

<212> DNA

<213> Arabidopsis thaliana

<400> 11

cctggatcta aattaag

17

<210> 12

<211> 21

<212> DNA

<213> Arabidopsis thaliana

<400> 12

tcgacttaat ttagatccag g

21

<210> 13

<211> 5

<212> PRT

<213> Arabidopsis thaliana

<400> 13

Leu Asp Leu Asn Leu

1

5

<210> 14

<211> 20

<212> DNA

<213> Arabidopsis thaliana

<400> 14

cctggatcta aatctgtaag

20

<210> 15

<211> 24

<212> DNA

<213> Arabidopsis thaliana

<400> 15

tcgacttaca gatttagatc cagg

24

<210> 16

<211> 10

<212> PRT

<213> Arabidopsis thaliana

<400> 16

Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala

1

5

10

<210> 17

<211> 35

<212> DNA

<213> Arabidopsis thaliana

<400> 17

cctggatcta gaactccgtt tgggtttcgc ttaag

35

<210> 18

<211> 39

<212> DNA

<213> Arabidopsis thaliana

<400> 18

tcgacttaag cgaaacccaa acggagtctt agatccagg

39

<210> 19

<211> 8

<212> PRT

<213> Arabidopsis thaliana

<400> 19

Leu Asp Leu Glu Leu Gly Phe Ala

1

5

<210> 20

<211> 39

<212> DNA

<213> Arabidopsis thaliana

<400> 20

cctggatcta gaactcgggtt tcgcttaag

39

<210> 21

<211> 43

<212> DNA

<213> Arabidopsis thaliana

<400> 21

tcgacttaag cgaaaccgag ttctagatcc agg

43

<210> 22

<211> 11

<212> PRT

<213> Arabidopsis thaliana

<400> 22

Leu Glu Leu Asp Leu Ala Ala Ala Ala Ala

1

5

10

<210> 23

<211> 38

<212> DNA

<213> Arabidopsis thaliana

<400> 23

actggaacta gatctagctg cagctgcagc tgcttaag

38

<210> 24

<211> 42

<212> DNA

<213> Arabidopsis thaliana

<400> 24

tcgacttaag cagctgcagc tgcagctaga tctagttcca gt

42

<210> 25

<211> 65

<212> DNA

<213> Cauliflower mosaic virus

<400> 25

agcttagatc tgcaagaccc ttctctata taaggaagtt catttcattt ggagaggaca 60

cgctg

65

<210> 26

<211> 65

<212> DNA

<213> Cauliflower mosaic virus

<400> 26

gatccagcgt gtctctcca aatgaaatga acttccttat atagaggaag ggtcttgcag 60

atcta

65

<210> 27

<211> 24

<212> DNA

<213> Cauliflower mosaic virus

<400> 27

cgccagggtt ttcccgatca cgac

24

<210> 28

<211> 37

<212> DNA

<213> Cauliflower mosaic virus

<400> 28

aagggtaacg ttaaggatag tgggatgtg cgtcatc

37

<210> 29

<211> 19

<212> DNA

<213> Arabidopsis thaliana

<400> 29

gatggagaga tcaaacagc

19

<210> 30

<211> 32

<212> DNA

<213> Arabidopsis thaliana

<400> 30

gataaagtta ttaccgtcga ctttaagcgaa ac

32

<210> 31

<211> 615



<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) (615)

<223>

<300>

<301> Sakai, H., Medrano, L. J. and Meyerowitz, E. M.

<302> Role of SUPERMAN in maintaining Arabidopsis floral whorl boundaries

<303> Nature

<304> 378

<305> 6553

<306> 199-203

<307> 1995

<308> U38946

<400> 31

atg gag aga tca aac agc ata gag tgg agg aac agc ttc tat ggc cgt 48

Met Glu Arg Ser Asn Ser Ile Glu Leu Arg Asn Ser Phe Tyr Gly Arg

1 5 10 15

gca aga act tca cca tgg agc tat gga gat tat gat aat tgc caa cag 96

Ala Arg Thr Ser Pro Trp Ser Tyr Gly Asp Tyr Asp Asn Cys Gln Gln

20 25 30

gat cat gat tat ctt cta ggg ttt tca tgg cca cca aga tcc tac act 144

Asp His Asp Tyr Leu Leu Gly Phe Ser Trp Pro Pro Arg Ser Tyr Thr

35 40 45

tgc agc ttc tgc aaa agg gaa ttc aga tcg gct caa gca ctt ggt ggc 192

Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala Leu Gly Gly

50 55 60

cac atg aat gtt cac aga aga gac aga gca aga ctc aga tta caa cag 240

His Met Asn Val His Arg Arg Asp Arg Ala Arg Leu Arg Leu Gln Gln

65	70	75	80
tct cca tca tca tct tca aca cct tct cct cct tac cct aac cct aat	288		
Ser Pro Ser Ser Ser Ser Thr Pro Ser Pro Pro Tyr Pro Asn Pro Asn			
85	90	95	
tac tct tac tca acc atg gca aac tct cct cct cct cat cat tct cct	336		
Tyr Ser Tyr Ser Thr Met Ala Asn Ser Pro Pro Pro His His Ser Pro			
100	105	110	
cta acc cta ttt cca acc ctt tct cct cca tcc tca cca aga tat agg	384		
Leu Thr Leu Phe Pro Thr Leu Ser Pro Pro Ser Ser Pro Arg Tyr Arg			
115	120	125	
gca ggt ttg atc cgt tcc ttg agc ccc aag tca aaa cat aca cca gaa	432		
Ala Gly Leu Ile Arg Ser Leu Ser Pro Lys Ser Lys His Thr Pro Glu			
130	135	140	
aac gct tgt aag act aag aaa tca tct ctt tta gtg gag gct gga gag	480		
Asn Ala Cys Lys Thr Lys Lys Ser Ser Leu Leu Val Glu Ala Gly Glu			
145	150	155	160
gct aca agg ttc acc agt aaa gat gct tgc aag atc ctg agg aat gat	528		
Ala Thr Arg Phe Thr Ser Lys Asp Ala Cys Lys Ile Leu Arg Asn Asp			
165	170	175	
gaa atc atc agc ttg gag ctt gag att ggt ttg att aac gaa tca gag	576		
Glu Ile Ile Ser Leu Glu Leu Glu Ile Gly Leu Ile Asn Glu Ser Glu			
180	185	190	
caa gat ctg gat cta gaa ctc cgt ttg ggt ttc gct taa	615		
Gln Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala			
195	200		

<210> 32

<211> 18

<212> DNA

<213> Arabidopsis thaliana

<400> 32

gaatgatgaa atcatcag

18

<210> 33

<211> 29

<212> DNA

<213> Arabidopsis thaliana

<400> 33

catggcgact cctaacgaag tatctgcac

29

<210> 34

<211> 39

<212> DNA

<213> Arabidopsis thaliana

<400> 34

atcggttcaaa aactcaaggc taactaatca acaacggtc

39

<210> 35

<211> 65

<212> DNA

<213> Cauliflower mosaic virus

<400> 35

agcttagatc tgcaagaccc ttcctctata taaggaagtt catttcattt ggagaggaca 60

cgctg

65

<210> 36

<211> 65

<212> DNA

<213> Cauliflower mosaic virus

<400> 36

gatccagcgt gtcctctcca aatgaaatga acttccttat atagaggaag ggtcttgag 60  
atcta 65

<210> 37

<211> 24

<212> DNA

<213> Cauliflower mosaic virus

<400> 37

cgccagggtt ttcccagtcg cgac 24

<210> 38

<211> 37

<212> DNA

<213> Cauliflower mosaic virus

<400> 38

aagggtaacg ttaaggatag tgggattgtg cgtcatc 37

<210> 39

<211> 44

<212> DNA

<213> Artificial

<400> 39

gatcagccgc cgatcagccg ccgatcagcc gccgatcagc cgcc 44

<210> 40

<211> 44

<212> DNA

<213> Artificial

<400> 40

tcggccggct agtcggcggc tagtcggcgg ctatcggcgg ggatc 44

<210> 41

<211> 76

<212> DNA

<213> Artificial

<400> 41

gatccacaat taccaacaac aacaaacaac aaacaacatt acaattacag atccccgggg 60  
taccgtcgac gagctc 76

<210> 42

<211> 70

<212> DNA

<213> Artificial

<400> 42

cgtcgacggg acccccggga tcgtgaattg taatgttgtt tgttgtttgt tgttgttgtt 60  
ggtaattgtg 70

<210> 43

<211> 21

<212> DNA

<213> Arabidopsis thaliana

<400> 43

aatgatgttt aatgagatgg g 21

<210> 44

<211> 22

<212> DNA

<213> Arabidopsis thaliana

<400> 44

atgaatcccc gggatattat tc 22

<210> 45

<211> 19

<212> DNA

<213> Arabidopsis thaliana

<400> 45

cgacactgca gatcacaac

19

<210> 46

<211> 30

<212> DNA

<213> Arabidopsis thaliana

<400> 46

atcccggaacc atatggatac atcttgctgc

30

<210> 47

<211> 24

<212> DNA

<213> Arabidopsis thaliana

<400> 47

agtgggtcct actgtgtcgg actc

24

<211> 48

<212> 39

<213> DNA

<400> 48

ccaaataaca ttatcggtcg actcaaaatt ccataggtg

39

<210> 49

<211> 35

<212> PRT

<213> Nicotiana tabacum

<400> 49

Val Gly Pro Thr Val Ser Asp Ser Ser Ser Ala Val Glu Glu Asn Gly

1

5

10

15

Tyr Asp Gly Lys Arg Asp Ile Ala Leu Ala Leu Asn Leu Ala Pro Pro

20

25

30

Met Glu Phe

35

<210> 50

<211> 111

<212> DNA

<213> Nicotiana tabacum

<400> 50

agtgggtcct actgtgtcgg actgcctc tgcagtggaa gagaaccaat atgatgggga 60

aaagaggaat tgatcttgat cttaaccttg ctccacctat ggaatttga g 111

<210> 51

<211> 116

<212> DNA

<213> Nicotiana tabacum

<400> 51

tcgactcaaa attccatagg tggagcaagg ttaagatcaa gatcaattcc tcttttcccc 60

catcatattg gttctcttcc actgcagagg acgagtcgga cacagtagga cccact 116

<210> 52

<211> 1887

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) (1887)

<223>

<300>

<301>

Chao, Q., Rothenberg, M., Solano, R., Roman, G., Terzaghi, W. and Ecker, J. R.

<302>

Activation of the ethylene gas response pathway in Arabidopsis by the nuclear protein  
ETHYLENE-INSENSITIVE3 and related proteins

<303> Cell

<304> 89

<305> (7)

<306> 1133-1144

<307> (1997)

<308> AF004216

<400> 52

atg atg ttt aat gag atg gga atg tgt gga aac atg gat ttc ttc tct 48

Met Met Phe Asn Glu Met Gly Met Cys Gly Asn Met Asp Phe Phe Ser

1 5 10 15

tct gga tca ctt ggt gaa gtt gat ttc tgt cct gtt cca caa gct gag 96

Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu

20 25 30

cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt 144

Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val

35 40 45

gat gaa ttg gag agg agg atg tgg aga gac aaa atg cgg ctt aaa cgt 192

Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg

50 55 60

ctc aag gag cag gat aag ggt aaa gaa ggt gtt gat gct gct aaa cag 240



Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln  
 65                      70                      75                      80  
 agg cag tct caa gag caa gct agg agg aag aaa atg tct aga gct caa 288  
 Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln  
                     85                      90                      95  
 gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa gct 336  
 Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala  
                     100                      105                      110  
 caa ggc ttt gtt tat ggg att att ccg gag aat ggg aag cct gtg act 384  
 Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr  
                     115                      120                      125  
 ggt gct tct gat aat tta agg gag tgg tgg aaa gat aag gtt agg ttt 432  
 Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe  
                     130                      135                      140  
 gat cgt aat ggt cct gcg gct att acc aag tat caa gcg gag aat aat 480  
 Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn  
                     145                      150                      155                      160  
 atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat 528  
 Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His  
                     165                      170                      175  
 acc ttg caa gag ctt caa gac acg act ctt gga tcg ctt ttg tct gcg 576  
 Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala  
                     180                      185                      190  
 ttg atg caa cac tgt gat cct cct cag aga cgt ttt cct ttg gag aaa 624  
 Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys  
                     195                      200                      205  
 gga gtt cct cct ccg tgg tgg cct aat ggg aaa gag gat tgg tgg cct 672  
 Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro  
                     210                      215                      220  
 caa ctt ggt ttg cct aaa gat caa ggt cct gca cct tac aag aag cct 720

Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro  
 225                      230                      235                      240  
 cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc 768  
 His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile  
                     245                      250                      255  
 aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa 816  
 Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln  
                     260                      265                      270  
 tct aaa tgt ttg cag gat aag atg act gct aaa gag agt gct acc tgg 864  
 Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp  
                     275                      280                      285  
 ctt gct att att aac caa gaa gag tcc ttg gct aga gag ctt tat ccc 912  
 Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro  
                     290                      295                      300  
 gag tca tgt cca cct ctt tct ctg tct ggt gga agt tgc tcg ctt ctg 960  
 Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu  
 305                      310                      315                      320  
 atg aat gat tgc agt caa tac gat gtt gaa ggt ttc gag aag gag tct 1008  
 Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser  
                     325                      330                      335  
 cac tat gaa gtg gaa gag ctc aag cca gaa aaa gtt atg aat tct tca 1056  
 His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser  
                     340                      345                      350  
 aac ttt ggg atg gtt gct aaa atg cat gac ttt cct gtc aaa gaa gaa 1104  
 Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu  
                     355                      360                      365  
 gtc cca gca gga aac tcg gaa ttc atg aga aag aga aag cca aac aga 1152  
 Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg  
                     370                      375                      380  
 gat ctg aac act att atg gac aga acc gtt ttc acc tgc gag aat ctt 1200

Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu  
 385                                      390                                      395                                      400  
 ggg tgt gcg cac agc gaa atc agc cgg gga ttt ctg gat agg aat tcg 1248  
 Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser  
    405                                      410                                      415  
 aga gac aac cat caa ctg gca tgt cca cat cga gac agt cgc tta ccg 1296  
 Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro  
    420                                      425                                      430  
 tat gga gca gca cca tcc agg ttt cat gtc aat gaa gtt aag cct gta 1344  
 Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val  
    435                                      440                                      445  
 gtt gga ttt cct cag cca agg cca gtg aac tca gla gcc caa cca att 1392  
 Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile  
    450                                      455                                      460  
 gac tta acg ggt ata gtt cct gaa gat gga cag aag atg atc tca gag 1440  
 Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu  
 465                                      470                                      475                                      480  
 ctc atg tcc atg tac gac aga aat gtc cag agc aac caa acc tct atg 1488  
 Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met  
    485                                      490                                      495  
 gtc atg gaa aat caa agc gtg tca ctg ctt caa ccc aca gtc cat aac 1536  
 Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn  
    500                                      505                                      510  
 cat caa gaa cat ctc cag ttc cca gga aac atg gtg gaa gga agt ttc 1584  
 His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe  
    515                                      520                                      525  
 ttt gaa gac ttg aac atc cca aac aga gca aac aac aac aac agc agc 1632  
 Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser  
    530                                      535                                      540  
 aac aat caa acg ttt ttt caa ggg aac aac aac aac aac aat gtg ttt 1696

Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe  
 545                      550                      555                      560  
 aag ttc gac act gca gat cac aac aac ttt gaa gct gca cat aac aac 1728  
 Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn  
                     565                      570                      575  
 aac aat aac agt agc ggc aac agg ttc cag ctt gtg ttt gat tcc aca 1776  
 Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr  
                     580                      585                      590  
 ccg ttc gac atg gcg tca ttc gat tac aga gat gat atg tcg atg cca 1824  
 Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro  
                     595                      600                      605  
 gga gta gta gga acg atg gat gga atg cag cag aag cag caa gat gta 1872  
 Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val  
                     610                      615                      620  
 tcc ata tgg ttc taa    1887  
 Ser Ile Trp Phe  
 625

<210> 53

<211> 678

<212> DNA, PRT

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1) (678)

<223>

<300>

<301> Ohme-Takagi, M. and Shinshi, H

<302>

Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive

element

<303> Plant Cell

<304> 7

<305> (2)

<306> 173-182

<307> 1995

<308> D38124

<400> 53

atg gct gtc aaa aat aag gtt agt aat ggc aat ctg aaa gga gga aat 48

Met Ala Val Lys Asn Lys Val Ser Asn Gly Asn Leu Lys Gly Gly Asn

1 5 10 15

gtg aaa aca gat gga gtt aag gag gtt cac tac aga ggt gta agg aag 96

Val Lys Thr Asp Gly Val Lys Glu Val His Tyr Arg Gly Val Arg Lys

20 25 30

agg cca tgg ggt cgg tat gca gct gaa atc cgt gac ccg ggt aag aag 144

Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly Lys Lys

35 40 45

agt cgg gtc tgg tta ggt act ttc gac acg gcg gaa gag gcg gct aag 192

Ser Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Lys

50 55 60

gcg tac gac acc gcc gct cga gag ttt cgt gga ccc aaa gca aaa act 240

Ala Tyr Asp Thr Ala Ala Arg Glu Phe Arg Gly Pro Lys Ala Lys Thr

65 70 75 80

aac ttc cct tca ccg acg gag aat cag agc cca agt cac agc agc acc 288

Asn Phe Pro Ser Pro Thr Glu Asn Gln Ser Pro Ser His Ser Ser Thr

85 90 95

gtg gag tcc tct agt gga gag aat ggt gtt cac gcg ccg cct cat gcg 336

Val Glu Ser Ser Ser Gly Glu Asn Gly Val His Ala Pro Pro His Ala

100 105 110

ccg ctc gag ctg gat ctc acg cgc cgt ctt ggc tcc gtt gct gca gat 384

Pro Leu Glu Leu Asp Leu Thr Arg Arg Leu Gly Ser Val Ala Ala Asp  
 115 120 125  
 ggc ggt gac aac tgt cgc cgt tct ggg gaa gtt ggg tac ccg att ttc 432  
 Gly Gly Asp Asn Cys Arg Arg Ser Gly Glu Val Gly Tyr Pro Ile Phe  
 130 135 140  
 cac cag cag ccg act gtg gcg gtt ctg cca aat ggc cag ccg gtt ctg 480  
 His Gln Gln Pro Thr Val Ala Val Leu Pro Asn Gly Gln Pro Val Leu  
 145 150 155 160  
 ctc ttt gat tct ttg tgg cgg gcg gga gtt gtt aac agg cct cag cct 528  
 Leu Phe Asp Ser Leu Trp Arg Ala Gly Val Val Asn Arg Pro Gln Pro  
 165 170 175  
 tac cat gta acg ccg atg ggg ttt aac ggc gtt aac gcc gga gtg ggt 576  
 Tyr His Val Thr Pro Met Gly Phe Asn Gly Val Asn Ala Gly Val Gly  
 180 185 190  
 cct act gtg tcg gac tcg tcc tct gca gtg gaa gag aac caa tat gat 624  
 Pro Thr Val Ser Asp Ser Ser Ser Ala Val Glu Glu Asn Gln Tyr Asp  
 195 200 205  
 ggg aaa aga gga att gat ctt gat ctt aac ctt gct cca cct atg gaa 672  
 Gly Lys Arg Gly Ile Asp Leu Asp Leu Asn Leu Ala Pro Pro Met Glu  
 210 215 220  
 ttt tga 678  
 Phe  
 225

<210> 54

<211> 933

<212> DNA, PRT

<213> Arabidopsis thaliana

<220>

<221>

<222> (1) (933)

<223>

<300>

<301> Takada, S., Hibara, K., Ishida, T., Tasaka, M.

<302>

The cup-shaped cotyledon1 of Arabidopsis regulates shoot apical meristem formation

<303> Development

<304> 128

<305>

<306> 1127-1135

<307> 2001

<308> AB049069

<400> 54

atg gat gtt gat gtg ttt aac ggt tgg ggg agg cca aga ttt gaa gat 48

Met Asp Val Asp Val Phe Asn Gly Trp Gly Arg Pro Arg Phe Glu Asp

5

10

15

gaa tcc ctt atg cca cct ggg ttt agg ttt cat cca act gat gaa gag 96

Glu Ser Leu Met Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu

20

25

30

ctg atc act tac tat ctc ctc aag aag gtt ctt gac tct aat ttc tct 144

Leu Ile Thr Tyr Tyr Leu Leu Lys Lys Val Leu Asp Ser Asn Phe Ser

35

40

45

tgt gcc gcc att tct caa gtt gat ctc aac aag tct gag cct tgg gag 192

Cys Ala Ala Ile Ser Gln Val Asp Leu Asn Lys Ser Glu Pro Trp Glu

50

55

60

ctt cct gag aaa gcg aaa atg ggg gag aag gag tgg tac ttc ttc aca 240

Leu Pro Glu Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Thr

65

70

75

80

cta aga gac cgt aaa tac cca acg gga ctg aga acg aac aga gca aca 288

Leu Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr

85	90	95
gaa gct ggt tac tgg aaa gcc act ggt aaa gac aga gag atc aaa agc 336		
Glu Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Glu Ile Lys Ser		
100	105	110
tca aag aca aaa tca ctt ctc ggg atg aag aaa act ctt gtc ttt tac 384		
Ser Lys Thr Lys Ser Leu Leu Gly Met Lys Lys Thr Leu Val Phe Tyr		
115	120	125
aaa ggc aga gct cct aaa gga gag aag agt tgt tgg gtc atg cat gag 432		
Lys Gly Arg Ala Pro Lys Gly Glu Lys Ser Cys Trp Val Met His Glu		
130	135	140
tat cgc ctt gac ggc aaa ttc tct tac cat tac att tcc tcc tcc gct 480		
Tyr Arg Leu Asp Gly Lys Phe Ser Tyr His Tyr Ile Ser Ser Ser Ala		
145	150	155
aag gat gaa tgg gtt ctc tgt aaa gtt tgt ctg aaa agc ggc gta gtt 528		
Lys Asp Glu Trp Val Leu Cys Lys Val Cys Leu Lys Ser Gly Val Val		
165	170	175
agt aga gag acg aac ttg atc tct tct tct tct tct tct gcc gtc acc 576		
Ser Arg Glu Thr Asn Leu Ile Ser Ser Ser Ser Ser Ser Ala Val Thr		
180	185	190
gga gag ttc tcc tct gcc ggt tct gca att gct ccg atc atc aat acc 624		
Gly Glu Phe Ser Ser Ala Gly Ser Ala Ile Ala Pro Ile Ile Asn Thr		
195	200	205
ttt gcg acg gag cac gtg tcc tgt ttc tcc aat aac tct gct gct cat 672		
Phe Ala Thr Glu His Val Ser Cys Phe Ser Asn Asn Ser Ala Ala His		
210	215	220
acc gat gcg agc ttt cat aca ttc ctt ccc gct cca ccg ccg tca ctg 720		
Thr Asp Ala Ser Phe His Thr Phe Leu Pro Ala Pro Pro Pro Ser Leu		
225	230	235
ccc cca cgt cag cca cgt cac gtc ggt gat ggc gtg gcg ttt ggt cag 768		
Pro Pro Arg Gln Pro Arg His Val Gly Asp Gly Val Ala Phe Gly Gln		



245 250 255  
 ttt ctg gat ttg gga tca tcg gga cag att gat ttc gat gca gca gca 816  
 Phe Leu Asp Leu Gly Ser Ser Gly Gln Ile Asp Phe Asp Ala Ala Ala

260 265 270  
 gca gcg ttc ttt ccg aat cta cct tct ctg cct ccc acg gtt ctt cct 864  
 Ala Ala Phe Phe Pro Asn Leu Pro Ser Leu Pro Pro Thr Val Leu Pro

275 280 285  
 cct cct ccg tca ttt gca atg tac ggt gga ggc tcc ccc gcc gtg agt 912  
 Pro Pro Pro Ser Phe Ala Met Tyr Gly Gly Gly Ser Pro Ala Val Ser

290 295 300  
 gtg tgg ccg ttt act ctc tga 933  
 Val Trp Pro Phe Thr Leu \*\*\*

305 310

<210> 55

<211> 60

<212> DNA

<213> Arabidopsis thaliana

<400> 55

ttaagcgaaa cccaaacgga gtctagatc cagatcgaga gtaaagggcc acacactcac 60

<210> 56

<211> 26

<212> DNA

<213> Arabidopsis thaliana

<400> 56

gggatggatg ttgatgtgtt taacgg

26

<210> 57

<211> 34

<212> DNA

<213> Arabidopsis thaliana

<400> 57

cctggatcta gaactccgtt tgggtttcgc ttaa

34

<210> 58

<211> 39

<212> DNA

<213> Arabidopsis thaliana

<400> 58

tcgacttaag cgaaacccaa acggagtctt agatccagg

39

<210> 59

<211> 37

<212> DNA

<213> Arabidopsis thaliana

<400> 59

cccttgatctta accttgctc cacctatgga attttga

37

<210> 60

<211> 42

<212> DNA

<213> Arabidopsis thaliana

<400> 60

tcgactcaaa attccatagg tggagcaagg ttaagatcaa gg

42

<210> 61

<211> 30

<212> PRT

<213> Arabidopsis thaliana

<400> 61

Asn Asp Glu Ile Ile Ser Leu Glu Leu Glu Ile Gly Leu Ile Asn Glu

1

5

10

15

Ser Glu Gln Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala

20

25

30

<210> 62

<211> 35

<212> DNA

<213> Arabidopsis thaliana

<400> 62

aaaatggagg gtctgtccaa agggctgcga aaagg

35

<210> 63

<211> 34

<212> DNA

<213> Arabidopsis thaliana

<400> 63

atcaaatttc acagtctctc catcgaaaag actc

34

<210> 64

<211> 40

<212> DNA

<213> Arabidopsis thaliana

<400> 64

ctggatctgg atctagaact ccgtttgggt ttcgcttaag

40

<210> 65

<211> 40

<212> DNA

<213> Arabidopsis thaliana

<400> 65

CTTAAGCGAA ACCCAAACGG AGTTCTAGAT CCAGATCCAG

40

<210> 66

<211> 747

<212> DNA, PRT

<213> Arabidopsis thaliana

<220>

<221>

<222> (1) (747)

<223>

<300>

<301> Borevitz J.O., Xia Y., Blount J., Dixon R.A., Lamb C.

<302>

Activation tagging identifies a conserved MYB regulator of phenylpropanoid biosynthesis.

<303> Plant Cell

<304> 12

<305>

<306> 2383-2393

<307> 2000

<308> AF325123

<400> 66

atg gag ggt tgc tcc aaa ggg ctg cga aaa ggt gct tgg act act gaa 48

MET Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu

1

5

10

15

gaa gat agt ctc ttg aga cag tgc att aat aag tat gga gaa ggc aaa 96

Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys

20	25	30	
tgg cac caa gtt cct gta aga gct ggg cta aac cgg tgc agg aaa agt	144		
Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser			
35	40	45	
tgt aga tta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga	192		
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly			
50	55	60	
aaa ctt agc tct gat gaa gtc gat ctt ctt ctt cgc ctt cat agg ctt	240		
Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu			
65	70	75	80
cta ggg aat agg tgg tct tta att gct gga aga tta cct ggt cgg acc	288		
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr			
85	90	95	
gca aat gac gtc aag aat tac tgg aac act cat ctg agt aag aaa cat	336		
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His			
100	105	110	
gaa ccg tgt tgt aag ata aag atg aaa aag aga gac att acg ccc att	384		
Glu Pro Cys Cys Lys Ile Lys MET Lys Lys Arg Asp Ile Thr Pro Ile			
115	120	125	
cct aca aca ccg gca cta aaa aac aat gtt tat aag cct cga cct cga	432		
Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg			
130	135	140	
tcc ttc aca gtt aac aac gac tgc aac cat ctc aat gcc cca cca aaa	480		
Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys			
145	150	155	160
gtt gac gtt aat cct cca tgc ctt gga ctt aac atc aat aat gtt tgt	528		
Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys			
165	170	175	
gac aat agt atc ata tac aac aaa gat aag aag aaa gac caa cta gtg	576		
Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val			

180	185	190	
aat aat ttg att gat gga gat aat atg tgg tta gag aaa ttc cta gag			624
Asn Asn Leu Ile Asp Gly Asp Asn MET Trp Leu Glu Lys Phe Leu Glu			
195	200	205	
gaa agc caa gag gta gat att ttg gtt cct gaa gcg acg aca aca gaa			672
Glu Ser Gln Glu Val Asp Ile Leu Val Pro Glu Ala Thr Thr Thr Glu			
210	215	220	
aag ggg gac acc ttg gct ttt gac gtt gat caa ctt tgg agt ctt ttc			720
Lys Gly Asp Thr Leu Ala Phe Asp Val Asp Gln Leu Trp Ser Leu Phe			
225	230	235	240
gat gga gag act gtg aaa ttt gat tag			747
Asp Gly Glu Thr Val Lys Phe Asp			
245			

<210> 67

<211> 34

<212> DNA

<213> Arabidopsis thaliana

<400> 67

aaaatgagaa tgacaagaga tggaaaagaa catg

34

<210> 68

<211> 34

<212> DNA

<213> Arabidopsis thaliana

<400> 68

aaggcaatac ccattagtaa aatccatcat agtg

34

<210> 69

<211> 660

<212> DNA, PRT

<213> Arabidopsis thaliana

<220>

<221>

<222> (1) (660)

<223>

<300>

<301> Kirik V., Schnittger A., Radchuk V., Adler K., Hulskamp M., Baumlein H.

<302>

Ectopic expression of the Arabidopsis AtMYB23 gene induces differentiation of trichome cells.

<303> Developmental Biology

<304> 235

<305>

<306> 366-377

<307> 2001

<308> Z68158

<400> 69

atg aga atg aca aga gat gga aaa gaa cat gaa tac aag aaa ggt tta 48

MET Arg MET Thr Arg Asp Gly Lys Glu His Glu Tyr Lys Lys Gly Leu

1

5

10

15

tgg aca gtt gaa gaa gac aag atc ctc atg gat tat gtc cga act cat 96

Trp Thr Val Glu Glu Asp Lys Ile Leu MET Asp Tyr Val Arg Thr His

20

25

30

ggc cag ggc cac tgg aac cgc atc gcc aag aaa act ggg ctc aag aga 144

Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg

35

40

45

tgt ggg aaa agc tgt agg ttg aga tgg atg aac tac tta agc cct aat 192

Cys Gly Lys Ser Cys Arg Leu Arg Trp MET Asn Tyr Leu Ser Pro Asn

50

55

60

gtt aac aga ggc aat ttt act gac caa gaa gaa gat ctc atc atc aga	240
Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg	
65 70 75 80	
ctc cac aag ctc ctc ggc aac aga tgg tgc ttg ata gcg aaa aga gtt	288
Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val	
85 90 95	
ccg gga aga aca gac aac caa gta aag aat tac tgg aac aca cat ctc	336
Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu	
100 105 110	
agc aag aaa ctt ggt ctc gga gat cat tca act gcc gtc aaa gcc gca	384
Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala	
115 120 125	
tgc ggt gta gag tct cca ccg tct atg gcc ctt ata acc aca acg tcc	432
Cys Gly Val Glu Ser Pro Pro Ser MET Ala Leu Ile Thr Thr Thr Ser	
130 135 140	
tcc tct cat caa gag atc tcc ggt gga aaa aat tca act cta agg ttc	480
Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe	
145 150 155 160	
gac act tta gtt gac gaa tcc aaa ctc aaa cca aaa tcc aaa cta gtc	528
Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val	
165 170 175	
cac gca aca cca act gac gta gaa gtt gca gct acg gtt cca aat ctg	576
His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu	
180 185 190	
ttc gat acc ttt tgg gtt ctt gaa gac gac ttc gag ctt agt tca ctc	624
Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu	
195 200 205	
act atg atg gat ttt act aat ggg tat tgc ctt tga	660
Thr MET MET Asp Phe Thr Asn Gly Tyr Cys Leu	
210 215	



<210> 70

<211> 24

<212> DNA

<213> Arabidopsis thaliana

<400> 70

cgtggatcac agcaatacag agcc

24

<210> 71

<211> 25

<212> DNA

<213> Arabidopsis thaliana

<400> 71

cctcctgcac ttccaçttcg tcttc

25

<210> 72

<211> 20

<212> DNA

<213> Arabidopsis thaliana

<400> 72

aaaaagatga caggatgggt

20

<210> 73

<211> 20

<212> DNA

<213> Arabidopsis thaliana

<400> 73

cccctgtttc tgtcttgta

20

<210> 74

<211> 26

<212> DNA

<213> Arabidopsis thaliana

<400> 74

gggatggata attcagctcc agattc

26

<210> 75

<211> 22

<212> DNA

<213> Arabidopsis thaliana

<400> 75

aactctaagg agctgcattt tg

22

<210> 76

<211> 33

<212> DNA

<213> Arabidopsis thaliana

<400> 76

gggatgagaa taaggagaag agatgaaaaa gag

33

<210> 77

<211> 33

<212> DNA

<213> Arabidopsis thaliana

<400> 77

aaggcagtac tcaatatcac tagaagcaaa att

33

<210> 78

<211> 33

<212> DNA

<213> Arabidopsis thaliana

<400> 78

atggccgtcg acatgtcttc caaacaaccc acc

33

<210> 79

<211> 30

<212> DNA

<213> Arabidopsis thaliana

<400> 79

gcagggagtt ctcgtagcgt tcttgaatag

30

<210> 80

<211> 11

<212> PRT

<213> artificial

<400> 80

Leu Glu Leu Arg Leu Ala Ala Ala Ala Ala

1

5

10

<210> 81

<211> 41

<212> DNA

<213> artificial

<400> 81

actagaactc cgtttggctg ccgcagcggc tgcataatga g

41

<210> 82

<211> 45

<212> DNA

<213> artificial

<400> 82

tcgactcatt atgcagccgc tgcggcagcc aaacggagtt ctagt

45

<210> 83

<211> 6

<212> PRT

<213> artificial

<400> 83

Asp Leu Glu Leu Arg Leu

1

5

<210> 84

<211> 26

<212> DNA

<213> artificial

<400> 84

agatctagaa ctccgtttgt aatgag

26

<210> 85

<211> 30

<212> DNA

<213> artificial

<400> 85

tcgactcatt acaaacggag ttctagatct

30

<210> 86

<211> 10

<212> PRT

<213> artificial

<400> 86

Leu Asp Leu Gln Leu Arg Leu Gly Tyr Tyr

1

5

10

<210> 87

<211> 38

<212> DNA

<213> artificial

<400> 87

actggaicta caactccgtt tgggttatta ctaatgag

38

<210> 88

<211> 41

<212> DNA

<213> artificial

<400> 88

tcgactcatt agtaataacc caaacggagt tgtagatcca g

41

<210> 89

<211> 7

<212> PRT

<213> artificial

<400> 89

Leu Asp Leu Glu Leu Arg Leu

1

5

<210> 90

<211> 29

<212> DNA

<213> artificial

<400> 90

actggatcta gaactccgtt tgtaatgag

29

<210> 91

<211> 33

<212> DNA

<213> artificial

<400> 91

tgcactcatt acaaacggag ttctagatcc agt

33

<210> 92

<211> 11

<212> PRT

<213> artificial

<400> 92

Leu Asp Leu Glu Leu Ala Ala Ala Ala Ala Ala

1

5

10

<210> 93

<211> 41

<212> DNA

<213> artificial

<400> 93

actggatcta gaactcgctg ccgcagcggc tgcataatga g

41

<210> 94

<211> 45

<212> DNA

<213> artificial

<400> 94

tgcactcatt atgcagccgc tgcggcagcg agttctagat ccagt

45

<210> 95

<211> 10

<212> PRT

<213> artificial

<400> 95

Leu Asp Leu Glu Leu Arg Leu Ala Ala Ala

1

5

10

<210> 96

<211> 38

<212> DNA

<213> artificial

<400> 96

actggatcta gaactccgtt tggctgccgc ataatgag

38

<210> 97

<211> 42

<212> DNA

<213> artificial

<400> 97

tgcactcatt atgcggcagc caaacggagt tctagatcca gt

42

<210> 98

<211> 11

<212> PRT

<213> artificial

<400> 98

Leu Glu Leu Asp Leu Ala Ala Ala Ala Ala

1

5

10

<210> 99

<211> 38

<212> DNA

<213> artificial

<400> 99

ccttgagcct gatcttgctg ctgctgctgc tgcttgag

38

<210> 100

<211> 42

<212> DNA

<213> artificial

<400> 100

tcgactcaag cagcagcagc agcagcaaga tcaagctcaa gg

42

<210> 101

<211> 8

<212> PRT

<213> artificial

<400> 101

Leu Asp Leu Glu Leu Arg Leu Gly

1

5

<210> 102

<211> 26

<212> DNA

<213> artificial

<400> 102

cctggatcta gaactccgtg gttaag

26



<210> 103

<211> 30

<212> DNA

<213> artificial

<400> 103

tcgacttaac cacggagtc tagatccagg

30

<210> 104

<211> 5

<212> PRT

<213> artificial

<400> 104

Leu Glu Leu Arg Leu

1

5

<210> 105

<211> 23

<212> DNA

<213> artificial

<400> 105

tctagaactc cgtttgtaat gag

23

<210> 106

<211> 27

<212> DNA

<213> artificial

<400> 106

tcgactcatt acaaacggag ttctaga

27

<210> 107

<211> 11

<212> PRT

<213> artificial

<400> 107

Phe Asp Leu Asn Phe Ala Pro Leu Asp Cys Val

1

5

10

<210> 108

<211> 38

<212> DNA

<213> artificial

<400> 108

attcgatctt aattttgcac cgttggattg tgtttaag

38

<210> 109

<211> 45

<212> DNA

<213> artificial

<400> 109

tcgactcatt aaacacaatc caacggtgca aaattaagat cgaat

45

<210> 110

<211> 12

<212> PRT

<213> artificial

<400> 110

Phe Asp Leu Asn Ile Phe Pro Pro Ile Pro Glu Phe

1

5

10

<210> 111

<211> 38

<212> DNA

<213> artificial

<400> 111

gtttgacctc aacatccctc cgaaccctga attctaag

38

<210> 112

<211> 42

<212> DNA

<213> artificial

<400> 112

tcgacttaga attcagggat cggagggatg ttgaggtaaa ac

42

<210> 113

<211> 13

<212> PRT

<213> artificial

<400> 113

Phe Gln Phe Asp Leu Asn Phe Pro Pro Leu Asp Cys Val

1

5

10

<210> 114

<211> 44

<212> DNA

<213> artificial

<400> 114

ctttcaattc gatcttaatt ttccaccgtt ggattgtgtt taag

44

<210> 115

<211> 48

<212> DNA

<213> artificial

<400> 115

tcgacttaaa cacaatccaa cggtaggaaaa ttaagatcga attgaaag

48

<210> 116

<211> 6

<212> PRT

<213> artificial

<400> 116

Asp Leu Asp Leu Arg Leu

5

<210> 117

<211> 29

<212> DNA

<213> artificial

<400> 117

actggatcta gatctccgtt tgtaatgag

29

<210> 118

<211> 33

<212> DNA

<213> artificial

<400> 118

tcgactcatt acaaacggag atctagatcc agt

33